

Fig 1 (1)

1 tacaatgggg tggcggaggt gaagaaacgg ggttacttct atgctagaac gcaaggaaca 19ftf>

y n g v a e v k k r g y f y a r t
y n g v a e v n t e r q a n g q i

61 taaaaaatg tataaaagcg gtaaaaattg ggcagtcggt acactctcga ctgctgcgct
1 m y k s g k n w a v v t l s t a a

121 ggtatttggg gcaacaactg taaatgcac gcgggacaca aatattgaaa acaatgattc
18 l v f g a t t v n a s a d t n i e n n d

181 ttctactgta caagttacaa caggtgataa tgatattgct gttaaaagtg tgacacttgg
38 s s t v q v t t g d n d i a v k s v t l

241 tagtgggtcaa gttagtgcag ctagtgtac gactattaga acttctgcta atgcaaatag
58 g s g q v s a a s d t t i r t s a n a n

301 tgcttcttct gccgctaata cacaaaattc taacagtcaa gtagcaagtt ctgctgcaat
78 s a s s a a n t q n s n s q v a s s a a

361 aacatcatct acaagttccg cagcttcatt aaataacaca gatagtaaag cggctcaaga
98 i t s s t s s a a s l n n t d s k a a q

421 aaatactaata acagccaaaa atgatgacac gcaaaaagct gcaccagcta acgaatcttc
118 e n t n t a k n d d t q k a a p a n e s

481 tgaagctaaa aatgaaccag ctgtaaactg taatgattct tcagctgcaa aaaatgatga
138 s e a k n e p a v n v n d s s a a k n d

541 tcaacaatcc agtaaaaaga atactaccgc taagttaaac aaggatgctg aaaacgttgt
158 d q q s s k k n t t a k l n k d a e n v

601 aaaaaaggcg ggaattgatc ctaacagttt aactgatgac cagattaaag cattaaataa
178 v k k a g i d p n s l t d d q i k a l n

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Fig 1 (2)

661 gatgaacttc tcgaaagctg caaagtctgg tacacaaatg acttataatg atttccaaaa
198 k m n f s k a a k s g t q m t y n d f q

721 gattgctgat acgttaatca aacaagatgg tcggtacaca gttccattct ttaaagcaag 20ftfi <
218 k i a d t l i k q d g r y t v p f f k a

781 tgaaatcaaa aatatgcttg ccgctacaac taaagatgca caaactaata ctattgaacc
238 s e i k n m p a a t t k d a q t n t i e

841 tttagatgta tgggattcat ggccagttca agatgttcgg acaggacaag ttgctaattg 5ftf >
258 p l d v w d s w p v q d v r t g q v a n 8ftfi <

901 gaatggctat caacttgtca tcgcaatgat gggaattcca aacccaaatg ataatcatat
278 w n g y q l v i a m m g i p n q n d n h

961 ctatctctta tataataagt atggtgataa tgaattaagt cattggaaga atgtaggctc 7ftf >
298 i y l l y n k y g d n e l s h w k n v g

1021 aatttttggc tataattcta ccgcggttcc acaagaatgg tcaggatcag ctgttttgaa 7ftf >
318 p i f g y n s t a v s q e w s g s a v l 6ftfi <

1081 cagtataac tctatccaat tattttatac aagggtagac acgtctgata acaataccaa
338 n s d n s i q l f y t r v d t s d n n t

1141 tcatcaaaaa attgctagcg ctactcttta ttttaactgat aataatggaa atgtatcact NheI
358 n h q k i a s a t l y l t d n n g n v s AC1(i)<>

1201 cgctcaggta cgaaatgact atattgtatt tgaaggtgat ggctattact accaaactta AC2(i)<>
378 l a q v r n d y i v f e g d g y y y q t

1261 tgatcaatgg aaagctacta acaaaggtgc cgataatatt gcaatgcgtg atgctcatgt
398 y d q w k a t n k g a d n i a m r d a h

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Fig 1 (3)

1321 aattgaagat ggtaatggtg atcggtacct tgtttttgaa gcaagtactg gtttgaaaa
418 v i e d g n g d r y l v f e a s t g l e

1381 ttatcaaggc gaggacaaa tttataactg gttaaattat ggcggagatg acgcatttaa
438 n y q g e d q i y n w l n y g g d d a f

1441 tatcaagagc ttatttagaa ttctttccaa tgatgatatt aagagtcggg caacttgggc
458 n i k s l f r i l s n d d i k s r a t w

1501 taatgcagct atcggtatcc tcaactaaa taaggacgaa aagaatccta aggtggcaga
478 a n a a i g i l k l n k d e k n p k v a

1561 gttataactca ccattaattt ctgcaccaat ggtaagcgat gaaattgagc gaccaaattg
498 e l y s p l i s a p m v s d e i e r p n

1621 agttaaatta ggtaataaat attacttatt tgccgctacc cgtttaaatc gaggaagtaa
518 v v k l g n k y y l f a a t r l n r g s

1681 tgatgatgct tggatgaatg ctaattatgc cggtggtgat aatggtgcaa tggtcggata
538 n d d a w m n a n y a v g d n v a m v g

1741 tgttgctgat agtctaactg gatcttataa gccattaaat gattctggag tagtcttgac
558 y v a d s l t g s y k p l n d s g v v l

1801 tgcttctggt cctgcaaact ggoggacagc aacttattca tattatgctg tccccgttgc
578 t a s v p a n w r t a t y s y y a v p v

1861 cggaaaagat gaccaagtat tagttacttc atatatgact aatagaaatg gagtagcggg
598 a g k d d q v l v t s y m t n r n g v a

1921 taaaggaatg gattcaactt gggcaccgag tttcttacta caaattaacc cggataaac 12ftfi <
618 g k g m d s t w a p s f l l q i n p d n

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Fig 1 (4)

1981 aactactgtt ttagctaaaa tgactaatca aggggattgg atttgggatg attcaagcga
638 t t t v l a k m t n q g d w i w d d s s

2041 aaatcttgat atgattgggtg atttagactc cgctgcttta cctggcgaac gtgataaacc
658 e n l d m i g d l d s a a l p g e r d k

2101 tgttgattgg gacttaattg gttatggatt aaaaccgcat gatcctgcta caccaaata
678 p v d w d l i g y g l k p h d p a t p n

2161 tcctgaaacg ccaactacac cagaaacccc tgagacacct aatactccca aaacacccaaa
698 d p e t p t t p e t p e t p n t p k t p

2221 gactcctgaa aatcctggga cacctcaaac tcctaataca cctaatactc cggaattcc
718 k t p e n p g t p q t p n t p n t p e i

2281 tttaactcca gaaacgccta agcaacctga aacccaaact aataatcgtt tgccacaaac
738 p l t p e t p k q p e t q t n n r l p q

2341 tggaaataat gccataaag ccatgattgg cctaggtatg ggaacattgc ttagtatgtt
758 t g n n a n k a m i g l g m g t l l s m

2401 tggctcttgca gaaattaaca aacgtcgatt taactaaata ctttaaaata aaaccgctaa
778 f g l a e i n k r r f n -

2461 gccttaaatt cagcttaacg gttttttatt ttaaaagttt ttattgtaaa aaagcgaatt

2521 atcattaata ctaatgcaat tgttgtaaga ccttacgaca gtagtaacaa tgaatttgc

2581 catctttgtc gg

NheI

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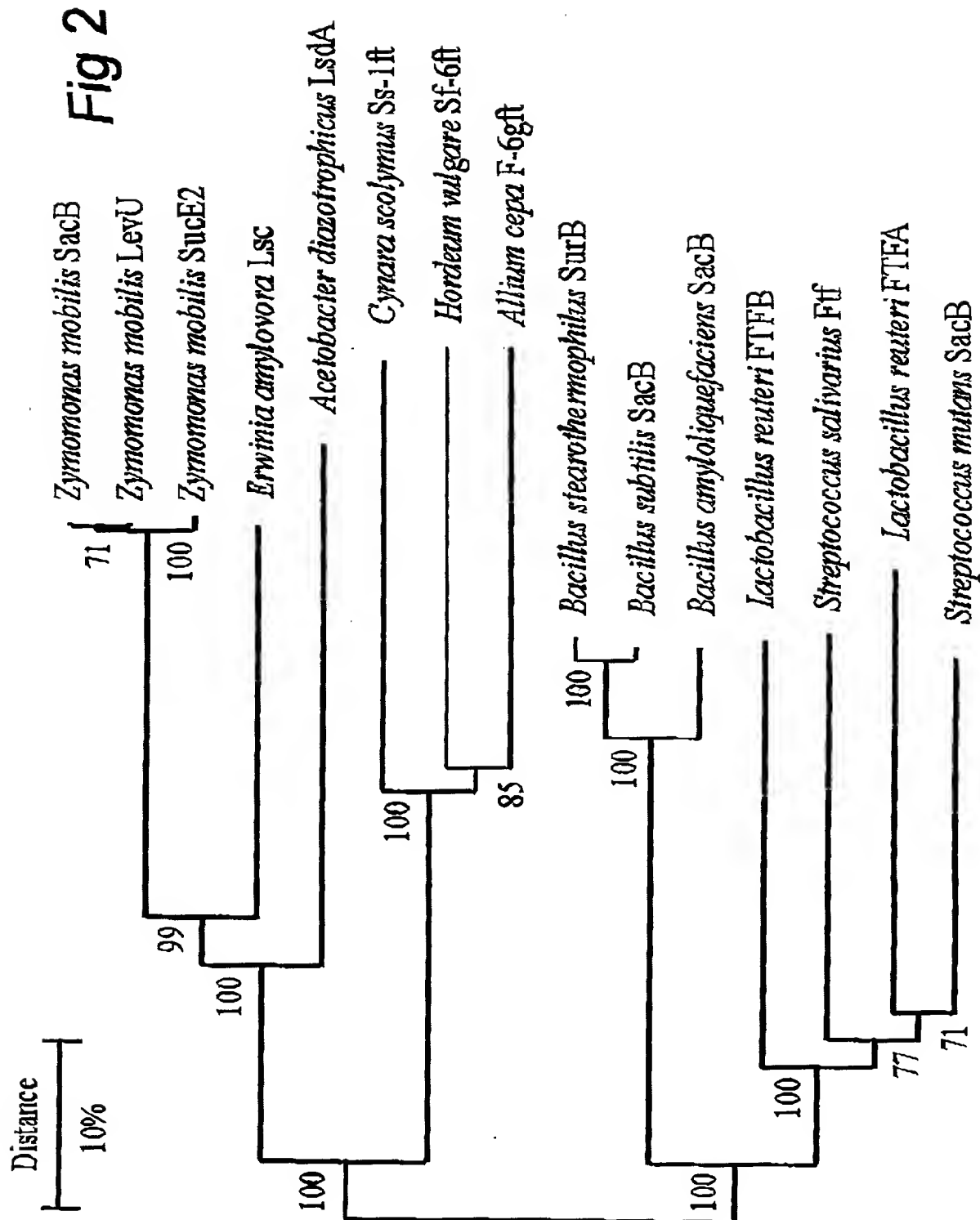


Fig 3

The N-terminal sequence of FTFB (levansucrase):

(A) Q V E S N N Y N G V A E V N T E R Q A N G Q I (G) (V) (D).

Internal peptide sequences of FTFB (levansucrase):

- (M) (A) H L D V W D S W P V Q D P (V),
- N A G S I F G T (K),
- V (E) (E) V Y S P K V S T L M A S D E V E.

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Fig 4

5ftf				
<i>B. amyloliquefaciens</i> SacB	80	GLDVWDSWPQNAD	93	
<i>B. subtilis</i> SacB	82	GLDVWDSWPQNAD	95	
<i>S. mutans</i> SacB	243	DLDVWDSWPVQDAK	256	
<i>S. salivarius</i> Ftf	282	EIDVWDSWPVQDAK	295	
		:*****:*:*.		
6ftfi				
<i>B. amyloliquefaciens</i> SacB	156	QTQWNGSATFTSDGK	171	
<i>B. subtilis</i> SacB	158	QTQWNGSATFTSDGK	173	
<i>S. mutans</i> SacB	312	LTQWNGSATVNEDEGS	327	
<i>S. salivarius</i> Ftf	351	DDQQWNGSATVNSDGS	366	
		*:*****...**.		
12ftfi				
<i>B. amyloliquefaciens</i> SacB	440	KATFGPSFLMN	450	
<i>B. subtilis</i> SacB	440	QSTFAPSFLN	450	
<i>S. mutans</i> SacB	609	NSTWAPSFLIQ	619	
<i>S. salivarius</i> Ftf	655	KSTWAPSFLIK	665	
		::*:.*****::		

Fig 5

